

## FIGURE 1

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTG  
AGAAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGAC  
CC

><MET {trans=1-s, dir=f, res=1}

ATGCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTC  
CTTGGCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCC  
GGAGCCCTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGC  
TGGGTCCAGCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAA  
CTGGCTCAAGCCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTG  
TGGCGCACCCCTGCAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGGCTTGGCGTCTTTT  
GTTGAAGTGGTCAGCCTATGGTTTGCAGAGGGGGCAGCGGTACAGCCACGCGGCAGGAGAG  
TGTGCTCGCAACGCCACCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAG  
CTGGGCTGTGGGCGGCACCTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGT  
GCCTACTCCCCCGGAGGCAACTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAG  
GGTGCCTGGTGTTCGCTCTGCACAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCAT  
GCAGGGGGGCTCTGTGAGGTCCCCAGGAATCCTTGTCGCATGAGCTGCCAGAACCATGGA  
CGTCTCAACATCAGCACCTGCCACTGCCACTGTCCCCCTGGCTACACGGGCAGATACTGC  
CAAGTGAGGTGCAGCCTGCAGTGTGTGCACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGC  
GTCTGTGACATCGGCTACGGGGGAGCCCAGTGTGCCACCAAGGTGCATTTTCCCTTCCAC  
ACCTGTGACCTGAGGATCGACGGAGACTGCTTCATGGTGTCTTCAGAGGCAGACACCTAT  
TACAGAGCCAGGATGAAATGTCAGAGGAAAGCGGGGTGCTGGCCCAGATCAAGAGCCAG  
AAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCCGCCTGGAGACCACCAACGAGGTGACT  
GACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCTCACCTACAAGACCGCCAAGGAC  
TCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCAGTTTTGCCTTTGGGCAGCCT  
GACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTTGGCAACTGCGTGGAGCTG  
CAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATC  
TGCCAGTTTGGCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACA  
TGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGCCACCTGTCTGG  
AACAAGGGCCAGGTAAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAA  
TGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTGAGTGTTAG  
AGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGATGGCGA  
AGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGACCCTG  
TGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAGCT  
GAAAAAAAAAAAAA

# FIGURE 2

1 CTCTTTTGTG CACCAGCCCA GCCTGACTCC TGGAGATTGT GAATAGCTCC ATCCAGCCTG AGAAACAAGC CGGGTGGCTG AGCCAGGCTG TGCACGGAGC  
GAGAAAAACAG GTGGTCGGGT CGGACTGAGG ACCTCTAACA CTATATCGAGG TAGGTTCGGAC TCTTTGTTCTG GCGCCACGAC TCGGTCCGAC ACCTGCTCTG

101 ACCTGACGGG CCCAACAGAC CCATGCTGCA TCCAGAGACC TCCCTGGGCC GGGGGCATCT CCTGGCTGTG CTCCTGGCCC TCCTTGGCAC CACCTGGGCA  
TGGACTGCCG GGGTTGTCTG CGTACGACGT AGTCTCTCTG AGGGGACCGG CCGGCTAGTA GGACCGACAC GAGGACCGGG AGGAACCGTG GTGGACCGCT

1 M L H P E T S P G R G H L L A V L L A L L G T T W A  
\*MET

201 GAGGTGTGGC CACCCAGCT GCAGGAGCAG GCTCCGATGG CCGGAGCCCT GAACAGGAAG GAGAGTTTCT TGCTCTCTCT CCTGCACAAC CGCCTGCGCA  
CTCCACACCG GTGGGGTCTGA CGTCTCTGTC CGAGGCTACC GGCCTCGGGA CTGTCTCTTC CTCTCAAAGA ACGAGGAGAG GGACGTGTG GCGGACCGCT

27 E V W P P Q L Q E Q A P M A G A L N R K E S F L L L S L H N R L R S

301 GCTGGGTCCA GCGCCCTGCG GCTGACATGC GGAGGCTGGA CTGGAGTGGC AGCCTGGCCC AACTGGCTCA AGCCAGGGCA GCGCTCTGTG GAATCCCAAC  
CGACCCAGGT CCGGGGACGC CGTCTGTACG CCTCCGACCT GACCTCACTG TCGGACGAGT TTGACCTCCG TCGGACGAGT CTTAGGGTTG

61 W V Q P P A A D M R R L D W S D S L A Q L A Q A R A A L C G I P T

401 CCGAGCCTG GCATCCGGCC TGTGGCGCAC CCTGCAAGTG GGCTGGAACA TGCAGTGTCT GCGCGCGGGC TTGGCGTCTT TTGTTGAAGT GGTACGCTA  
GGGCTCGGAC CGTAGGCGCG ACACCGCGTG GGACGTTTAC CCGACCTTGT ACGTCGACGA CCGGCGCGCG AACCGCAGGA AACAACTTCA CCAGTCCGAT

94 P S L A S G L W R T L Q V G W N M Q L L P A G L A S F V E V V S L

501 TGGTTTTCAG AGGGGACCGG GTACAGCCAC GCGGCAGGAG AGTGTGCTCG CAACGCCACC TGCACCCACT ACACCGAGCT CGTGTGGGCC ACCTCAAGCC  
ACCAAACGTC TCCCGTCCG CATGTCCGTTG CCGCGTCTCT TCACACGAGC GTTGGCGTGG ACGTGGGTGA TGTGCGTGA GCACACCGCG TGGAGTTCGG

127 W F A E G Q R Y S H A A G E C A R N A T C T H Y T Q L V W A T S S Q

601 AGCTGGGCTG TGGGCGGCAC CTGTGCTCTG CAGGCCAGAC AGCGATAGAA GCCTTTGTCT GTGCTACTCT CCGCGGAGGC AACTGGGAGG TCAACGGGAA  
TCGACCCGAC ACCCGCGTG GACACGAGAC GTCCGTTCTG TCGCTATCTT CCGAAACAGA CACGGATGAG GGGGCTCCG TTGACCTCTC AGTTGCCCTT

161 L G C G R H L C S A G Q T A I E A F V C A Y S P G G N W E V N G K

701 GACAATCATC CCCTATAAGA AGGGTGCCTG GTGTTGCTCT TGCACAGCCA GTGTCTCAGG CTGCTTCAAA GCCTGGGACC ATGCAGGGGG GCTCTGTGAG  
CTGTTAGTAG GGGATATCTT TCCACCGGAC CACAAGCGAG ACGTGTCCGT CACAGAGTCC GACGAAGTTT CCGACCTCTG TACGTCCCCC CGAGACACTC

194 T I I P Y K K G A W C S L C T A S V S G C F K A W D H A G G L C E

801 GTCCCCAGGA ATCCTTGTCT CATGAGCTGC CAGAACCATG GACGTCTCAA CATCACCACC TCCACTTGCC ACTGTCCCCC TGGCTACACG GGCAGATACT  
CAGGGGTCTT TAGGAACAGC GTACTCGAGC GTCTTGGTAC CTGCAAGATT GTAGTGTGGG ACGGTGACGG TGACAGGGGG ACCGATGTGC CCGTCTATGA

227 V P R N P Q R M S C Q N H G R L N I S T C H C H C P P G Y T H N R L R S

901 GCCAAGTGAG GTGCAGCCTG CAGTGTGTGC ACGGCGCGTT CCGGGAGGAG GAGTGTCTGT GCGTCTGTGA CATCGGCTAC GGGGAGCGCC AGTGTGCCAC  
CGGTTCACTC CACGTCCGAC GTACACACAG TGCAGGCGAA GCGCTCTCTC CTCACAGGCA CGCAGACACT GTAGCCGATG CCGCTCCGGG TCACACGGTG

261 Q V R C S L Q C V H G R F R E E E C S C V C D I G Y G G A Q C A T

1001 CAAGGTGCAT TTTCCCTTCC ACACCTGTGA CCTGAGGATC GACGGAGACT GCTTCATGGT GTCTTCAGAG GCAGACACCT ATTACAGAGC CAGGATGAAA  
GTTCCACGTA AAAGGGGAAGG TGTGGCACTT GGACTCTTAG CTGCTCTTGA CGAAGTACCA CAGAAGTCTC CGTCTGTGGA TAATGTCTCG GTCCCTACTTT

294 K V H F P F H T C D L R I D G D C F M V S S E A D T Y Y R A R M K

1101 TGTACAGGGA AAGGCGGGGT GCTGGCCCGC ATCAAGAGCC AGAAAGTGCA GGACATCTCT GCCTTCTATC TGGGCGCGCT GGAGACACCC AACGAGGTGA  
ACAGTCTCTT TTCCGCCCCA CAGCCGGGTC TAGTTCTCGG TCTTTACGTT CCGTAGGAG CCGAAGATAG ACCCGCGGGA CCTCTGTGTG TTGCTCCACT

327 C Q R K G G V L A Q I K S Q K V Q D I L A F Y L G R L E T T N E V T

1201 CTGACAGTGA CTTGAGAGAC AGGAACCTCT GGATCGGGCT CACCTACAAG ACCGCCAAGG ACTCCTTCCG CTGGGCCACA GGGGAGCACC AGGCCTTAC  
GACTGTCACT GAAGCTCTTG TCCTTGAAGA CCTAGCCCGA GTGGATGTTT TGGCGGTTCC TGAGGAAGGC GACCCGGTGT CCGCTCGTGG TCCGGAAGTG

361 D S D F E T R N F W I G L T Y K T A K D S F R W A T G E H Q A F T

1301 CAGTTTGTCC TTTGGGCAGC CTGACAACCA CCGGCTGGTG TGGCTGAGTG CTGCCATGGG GTTTGGCAAC TGGCTGGAGC TGCAGGCTTC AGCTGCTTTC  
GTCAAACCG AAACCCGTCG GACTGTGGT GCGCGACCA ACCGACTCAC GACGGTACCC CAACCGTTG ACGCACCTCG ACGTCCGAAG TCGACGGAAG

394 S F A F G Q P D N H G L V W L S A A M G F G N C V E L Q A S A A F

1401 AACTGGAACG ACCAGCGCTG CAAAACCCGA AACCGTTACA TCTGCCAGTT TGGCCAGGAG CACATCTCCC GGTGGGGCCC AGGGTCTCTA GGCCTGACCA  
TTGACCTTGC TGGTCCGCGC GTTTTGGGCT TTGGCAATGT AGACGGTCAA ACGGGTCTCT GTGTAGAGGG CCACCCCGGG TCCAGGACT CCGGACTGGT

427 N W N D Q R C K T R N R Y I C Q F A Q E H I S R W G P G S O

1501 CATGGCTCCC TCGCTGCCCC TGGGAGCACC GGCTCTGCTT ACCTGTCTGC CCACCTGTCT GGAACAAGGG CCAGGTAAAG ACCACATGCC TCATGTCCAA  
GTACCGAGGG AGCGGACGGG ACCCTCGTGG CCGAGACGAA TGGACAGAGC GGTGGACAGA CCTGTGTTCCC GGTCCAATTG TGGTGTACGG AGTACAGGTT

1601 AGAGGTCTCA GACCTTGCAC AATGCCAGAA GTTGGGCAGA GAGAGGCAGG GAGGCCAGTG AGGGCCAGGG AGTGAGTGTG AGAAGAAGCT GGGGCCCTTC  
TCTCCAGAGT CTGGAACGTG TTACGGTCTT CAACCCGTCT CTCTCCGTCC CTCCGGTCC TCCCGTCCC TCACTCACA TCTTCTTCGA CCGCGGGAAG

1701 GCGTGTCTTT GATTGGGAAG ATGGGCTTCA ATTAGATGGC GAAGGAGAGG ACACCGCCAG TGGTCCAAAA AGGCTGCTCT CTTCCACCTG GCCCAGACCC  
CGGACGAAAA CTAACCCCTC TACCCGAAGT TAATCTACCG CTTCCTCTCC TGTGGCGGTC ACCAGGTTTT TCCGACGAGA GAAGGTGGAC CCGGTCTGGG

1801 TGTGGGCGAG CCGAGCTTCC CTGTGGCATG AACCCACCGG GGTATTAAAT TATGAATCAG CTGAAAAAAA AAAAAA  
ACACCCCGTC GCCTCGAAGG GACACCGTAC TTGGGGTGCC CCATAATTTA ATACTTAGTC GACTTTTTTT TTTTTT

### **FIGURE 3**

><homology to cysteine-rich secretory proteins>

><signal peptide>

MLHPETSPGRGHLLAVLLALLGTTWA

><start mature protein>

EVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA  
QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAA  
GECAR

><potential N-glycosylation site>

NATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKK  
GAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRL

><potential N-glycosylation site>

NISTCH

><EGF-like domain cysteine pattern signature>

CHCPPGYTGRYCQVRCSLQCVHGRFREEECS

><EGF-like domain cysteine pattern signature>

CVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYRARMKCQRKGGVLA  
QIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAF  
TSFAFGQPDNHGLVWLSAAMGFGN

><C-type lectin domain signature (CVELQASAAFNWNDQRCKTRNRYIC)>

CVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS

# FIGURE 4

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
< 1 10 20 30 40 50 60 70
< | | | | | | | | | | | | | | |
MLHPETSPGRGHLAVLLALLGTTWAEVWPPQLQEQA PMAGALNRKESFLLLSLHNRLRSWVQPPAADMR
71 80 90 100 110 120 130 140
< | | | | | | | | | | | | | | |
RLDWSDSLQAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVS LWF AEGQRYSHAAGE
141 150 160 170 180 190 200 210
< | | | | | | | | | | | | | | |
CARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTAS
211 220 230 240 250 260 270 280
< | | | | | | | | | | | | | | |
VSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLLNISTCHCHCPPGYTG RY CQVRC SLQCVHGRFRREEECSC
281 290 300 310 320 330 340 350
< | | | | | | | | | | | | | | |
VCDIGYGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYRARMK CQRKGGVLAQIKSQKVQDILAFYL
351 360 370 380 390 400 410 420
< | | | | | | | | | | | | | | |
GRLETTNEVTDSDFE TRNFWIGLTYKTA KDSFRWATGEHQAF TSFAFGQPDNHGLVWLSAAMGFNCVEL
421 430 440 450
< | | | | | | | | | | | | | | |
QASAAFNWNDQRC KTRNRYICQFAQEHISRWGPGS

```

### FIGURE 5A

[illegible]

### FIGURE 5B

W79362	354	ATCACATGCCTCATGTGCCAAAGAAGGTCTCAGACTTTGCACAATGCCAGA
2554374	211	TGCCCTGTTGATGGCCTTGTACC-TGTGGGCTCCTGAGCCCAGAG
2992967	151	ATCACATGCCTCATGTGCCAAAGA-GGTCTCAGACCTTGCACAATGCCAGA
2673172	106	ACCACATGCCTCATGTGCCAAAGA-GGTCTCAGACCTTGCACAATGCCAGA
AA527105	1	GGTCGACCTTGCACAATGCCAGA
197200	1	ANTNCCAGA
<consen01>	351	..+..+.....+.. .++.....+...++..+.....+++++
		ATCACATGCCTCATGTGCCAAAGA GGTCTCAGACCTTGCACAATGCCAGA
W79362	404	AGTTGGGT
2992967	200	NGTTGGGCAGAGAGAGAGGCAGGGAGGCCAGTGAGGCC-AGG-AGTGAGTGT
2673172	155	AGTTGGGCAGAGAGAGAGGCAGGGAGGCCAGTGAGGGNAGGGAGTGANTGT
AA527105	24	AGTTGGGCAGAGAGAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGT
197200	10	NGTTGGGCAGAGAGAGAGGCAGGGAGGCCAGTNAGGGCCAGGCAGTGAGTNT
<consen01>	400	.+++++.+++++.....++++. .+++..++++.+.+
		AGTTGGGCAGAGAGAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGT
2992967	248	TAGAAGAAG-TGGGGN--TTCGNCTG-TTTTGNT-GGGA-G-TGGG-TTC
2673172	205	TAGAAGAAGCTGGGGTCCTTCGCCTGCTTTTGATTG
AA527105	74	TAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTC
197200	60	TAGACGAAGCTGGGGCCCNCGCCTNCTTTTNATTNGNNAGATGGGCTNN
<consen01>	450	++++.+++++.++++.+.+.+.+.++++. .+.+. .+++++..
		TAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTC
2992967	290	A-TTAGATGGC
AA527105	124	AATTAGATGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTC
197200	110	AATNAGATNGCGAAGGAGAGGACACCNCCANTGGTCCAAAAAGGCT
2127437	1	GAGGACACCGCCAGTGGTCCAAAAAGGCTGCTC
<consen01>	500	+++..++++.+++++.....++++. .+++++.....
		AATTAGATGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTC
AA527105	174	TCTTCCACCTGGCCCAGACCCTGTGGG-CAGCGGACTTCCCTGTGGCATG
2127437	34	TCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGACTTCCCTGTGGCATN
<consen01>	550	+++++.....
		TCTTCCACCTGGCCCAGACCCTGTGGGGCAGCGGACTTCCCTGTGGCATG
AA527105	223	AACCCACGGGTAATTAAATTATGAATCAGCTGAAAGAAGAAAAAGTCGG
2127437	84	AACCCACGGGGTATTAAATTATGAATCAGCTG
<consen01>	600	+++++.....
		AACCCACGGGTAATTAAATTATGAATCAGCTGAAAGAAGAAAAAGTCGG
AA527105	273	CG
<consen01>	650	++
		CG

## **FIGURE 6**

```
ACAGTGACTTCGAGACC
><39499.f1 {underline=1-24, dir=f}>
AGGAACCTTCTGGATCGGGCTCACCTACAAGACC
><39499.p1 {underline=1-45, dir=f}>
GCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTCACCAGTTTTGCCTTT
GGGCAGCCTGACAACCACGGGTTTGGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTC
AACTGGAACGACCAGCGCTGCAAAACCCGAAACCGTTACATCTGCCAGTTTGCCCAGGAG
CACATCTCCCGGTGGGGCCCAGGGTCCTGAGGCCTGACCACATGGCTCCCTCGCCTGCCC
TGGGAGCACCGGCTCTGCTTACCTGTCTGCCCACCTGTCTGGAACAAGGGCCAGGTTAAG
ATCACATGCCTCATGTCCAAAGAGGTCTCAGACCTTGCACAATGCCAGAAGTTGGGCAGA
GAGAGGCAGGGAGGCCAGTGAGGGCGAGGGAGTGAGTGTTAGAAGAAGCTGGGGCCCTTC
GCCTGCTTTTGGATTGGGAAGATGGGCTTCAATTAGATGGCGAAGGAGAGGACACCGCCAG
TGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGACC
><39499.r1 {underline=1-24, dir=b}>
CTGTGGGGCAGCGGACTTCCCTGTGGCATGAACCCACGGGTAATTAAATTATGAATCAG
CTGAAAGAAGAAAAAGTCGGCG
```

# FIGURE 7

```

1  ACAGTACTT CGAGACCAGG AACTTCTGGA TCGGGCTCAC CTACAAGACC GCCAAGACT CCTTCCGCTG GGCCACAGGG GAGCACCAGG CCTTCACCAG
   TGTCACCTGAA GCTCTGGTCC TTGAAGACCT AGCCCGAGTG GATGTTCTGG CCGTTCCTGA GGAAGCGGAC CCGGTGTCCC CTCGTGGTCC GGAAGTGGTC
   ^39499.f1
101 TTTTGGCCTTT GGCAGCCTG ACAACCACGG GTTTGGCAAC TCGGTGGAGC TGCAGGCTTC AGCTGCCCTTC AACTGGAAAG ACCAGCGCTG CAAAACCCGA
   AAAACGGAAA CCCGTCGGAC TGTGTTGGCC CAAACCGTTG ACGCACCTCG ACGTCCGAAG TCGACGGAAG TTGACCTTGC TGGTCGGAC GTTTTGGGCT
201 AACCGTTACA TCTGCCAGTT TGCCCCAGGAG CACATCTCCC GGTGGGGCCC AGGTTCTTGA GGCTTGACCA CATGGCTCCC TCGCCTGCCC TGGGAGCACC
   TTGGCAATGT AGACGGTCAA ACGGGTCTTC GTGTAGAGGG CCACCCCGGG TCCGACTGGT GTACCGAGGG AGCGGACGGG ACCCTCGTGG
301 GGCTCTGCTT ACCTGTCTGC CCACCTGTCT GGAACAAGGG CCAGGTTAAG ATCACATGCC TCATGTCCAA AGAGGTCTCA GACCTTGCAC AATGCCAGAA
   CCGAGACGAA TGGACAGACG GGTGGACAGA CCTTGTCTCC GGTCCAATTC TAGTGTACGG AGTACAGGTT TCTCCAGAGT CTGGAACGTG TTACGGTCTT
401 GTTGGGCAGA GAGAGGCAGG GAGGCCAGTG AGGGCGAGGG AGTGAGTGT AGAAGAAGCT GGGGCCCTTC GCCTGCTTTT GATTGGGAAG ATGGGCTTCA
   CAACCGTCT CTCTCCGTCC CTCCGCTCAC TCCCGTCCC TCACTCACA TCTTCTCTGA CCCCAGGAAG CGGACGAAAA CTAACCCCTTC TACCCGAAGT
501 ATTAGATGGC GAAGGAGAGG ACACCGCCAG TGGTCCAAAA AGGCTGCTCT CTTCACCTG GCCCAGACCC TGTGGGCAG CCGACTTCCC TGTGGCATGA
   TAATCTACCG CTTCTCTCTC TGTGGCGGTC ACCAGGTTT TCCGACGAGA GAAGTGGAC CCGGTCTGGG ACACCCGCTC GCCTGAAGGG ACACCGTACT
   ^39499.r1
601 ACCCCACGGG TAATTAAAT ATGAATCAGC TGAAGAAGA AAAAGTCGGC G
   TGGGTGCCC ATTAATTAA TACTTAGTCG ACTTCTTCT TTTTCAGCCG C

```



## FIGURE 8

```

>1 S68683 cysteine-rich secretory protein 3 precursor - human (245 aa)
Score = 235 (82.7 bits), Expect = 5.2e-18, P = 5.2e-18
Identities = 51/157 (32%), Positives = 78/157 (49%), at 273,42, Frame = +3

DNA44176 273 LLSLHNRLRSWVQPPAADMRRLLDWSDSLALQAQARAALCGIPTPSILASGLWRTLQVGWNN
S68683    ... ** ** * *** . * . . . . * ** * * * . . . * *
42 IVNKHNELRRRAVSPPARNMLKMEWNKEAANAQKWANQCNY-RHSNPKDRMTSLKCGENL

DNA44176 453 QLLPAGLASFEVVSILWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSA
S68683    . * . . . . ** * . * ** **** * . * . *** *
101 YMSSAS-SSWSQAIQSWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPN

DNA44176 633 GQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC
S68683    . . . . . * * * * . . . . . * *
160 QKVLKYYYVCQYCPAGNWA--NRLYVPYEQGAPCASC

```

## FIGURE 9

```

>8 ECCRISP3_1 cysteine-rich secretory protein-3 - Equus caballus (245 aa)
Score = 216 (76.0 bits), Expect = 5.8e-16, P = 5.8e-16
Identities = 71/242 (29%), Positives = 109/242 (45%), at 159,3, Frame = +3

DNA44176 159 LLAALLLGGTTWAEVWPPQLQEQAPMAGALNRKE-SFLLLSLHNRLRSWVQPPAADMRR
** *** * . * * * * * * * * * * * * * * * * * * * * * * *
ECCRISP3_1 3 LLPVLL-FLAAVLLPFFPASGQDPGFAALSITKSEVQKEIVNKHNDLRRITVSPLASNMLK

DNA44176 336 LDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWMMQLLPAGLASFVEVVSLEWFAEG
. * * * * * * * * * * * * * * * * * * * * * * * *
ECCRISP3_1 62 MQWDSKTATNAQNWANKCLLQHSKAEDRAVGTMKCGENL-FMSSIPNSWSDAIQNWHDDEV

DNA44176 516 QRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPPGNWEVN
. . * * * * * * * * * * * * * * * * * * * * * * *
ECCRISP3_1 121 HDFKYGVPKTPNAVVGHTYQVVMYSSYRVGCGIAYCPKQGTLYYYVVCQYCPAGNY-VN

DNA44176 696 GKTIIPTYKKGAWCS-----LCTAS-----VSGCFKAWDHAGGLCEVPRNPCRMSC
* **..* *. *** * ** * ** * ** * ** * ** * ** *
ECCRISP3_1 180 -KINTPYEQGTPCARCPGNCNDGLCTNSCEYEDLVSNCDSLKKIAGCEHELLKENCKTTC

DNA44176 831 QNHGRL
* ..
ECCRISP3_1 239 QCENKI

```

## FIGURE 10

>12 S68684 cysteine-rich secretory protein 1 precursor - human (249 aa)  
 Score = 207 (72.9 bits), Expect = 5.4e-15, P = 5.4e-15  
 Identities = 63/214 (29%), Positives = 96/214 (44%), at 273,44, Frame = +3

```

DNA44176 273 LLSLHNRLRSWVQPPAADMRRLDMSDSLQAQAARAALCGIPTPS-LASGLWRTLQVGWN
S68684 44 IVNIHNALRRRVVPPASNMLKMSWSEEAQNARIFSKYCDMTESNPLERRLPNTF-CGEN

DNA44176 450 MQLLPAGLASFVEVVSLLWFAEGQRYSHAAGECARN-ATCTHYTQLVWATSSQLGCGRHLG
S68684 103 MHMTSYPV-SWSSVIGVWYSESTSPKHGEWTTTDDDDITTDHYTQIVWATSYLIGCALASC

DNA44176 627 SAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVP
S68684 162 RQQGSPRYLIVCHYCHEGN-DPETKNE-PYKTGVPCEACP---SNC-----EDKLCT--

DNA44176 807 RNPGRMSQNHGRLNISTCHCHCPPGYTGRYCQVRC
S68684 209 -NPC-IYYDEYFDCDIQVHYLGCNHSHTILFCKATC

```